



ENTERED

PCT07

## RAW SEQUENCE LISTING

DATE: 03/07/2002

PATENT APPLICATION: US/09/830,338

TIME: 15:41:41

Input Set : A:\Ikeda Sequence Listing.txt

Output Set: N:\CRF3\03072002\I830338.raw

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3 <110> APPLICANT: IKEDA, Johe
4   SAKAI, Harumi
6 <120> TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory
Protein NAIP,
7   and Method For Assaying the NAIP
9 <130> FILE REFERENCE: 2001-0515A/WMC/00653
11 <140> CURRENT APPLICATION NUMBER: 09/830,338
C--> 12 <141> CURRENT FILING DATE: 2001-08-13
14 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05841
15 <151> PRIOR FILING DATE: 1999-10-22
17 <160> NUMBER OF SEQ ID NOS: 2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1403
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
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26     1             5             10             15
27   His Asn Leu Leu Pro Glu Leu Ser Ala Leu Leu Gly Leu Asp Ala Val
28           20             25             30
29   Gln Leu Ala Lys Glu Leu Glu Glu Glu Gln Lys Glu Arg Ala Lys
30           35             40             45
31   Met Gln Lys Gly Tyr Asn Ser Gln Met Arg Ser Glu Ala Lys Arg Leu
32           50             55             60
33   Lys Thr Phe Val Thr Tyr Glu Pro Tyr Ser Ser Trp Ile Pro Gln Glu
34           65             70             75             80
35   Met Ala Ala Ala Gly Phe Tyr Phe Thr Gly Val Lys Ser Gly Ile Gln
36           85             90             95
37   Cys Phe Cys Cys Ser Leu Ile Leu Phe Gly Ala Gly Leu Thr Arg Leu
38           100            105            110
39   Pro Ile Glu Asp His Lys Arg Phe His Pro Asp Cys Gly Phe Leu Leu
40           115            120            125
41   Asn Lys Asp Val Gly Asn Ile Ala Lys Tyr Asp Ile Arg Val Lys Asn
42           130            135            140
43   Leu Lys Ser Arg Leu Arg Gly Gly Lys Met Arg Tyr Gln Glu Glu
44           145            150            155            160
45   Ala Arg Leu Ala Ser Phe Arg Asn Trp Pro Phe Tyr Val Gln Gly Ile
46           165            170            175
47   Ser Pro Cys Val Leu Ser Glu Ala Gly Phe Val Phe Thr Gly Lys Gln
48           180            185            190
49   Asp Thr Val Gln Cys Phe Ser Cys Gly Gly Cys Leu Gly Asn Trp Glu
50           195            200            205
51   Glu Gly Asp Asp Pro Trp Lys Glu His Ala Lys Trp Phe Pro Lys Cys
52           210            215            220

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```

53  Glu Phe Leu Arg Ser Lys Lys Ser Ser Glu Glu Ile Thr Gln Tyr Ile
54  225                230                235                240
55  Gln Ser Tyr Lys Gly Phe Val Asp Ile Thr Gly Glu His Phe Val Asn
56  245                250                255
57  Ser Trp Val Gln Arg Glu Leu Pro Met Ala Ser Ala Tyr Cys Asn Asp
58  260                265                270
59  Ser Ile Phe Ala Tyr Glu Glu Leu Arg Leu Asp Ser Phe Lys Asp Trp
60  275                280                285
61  Pro Arg Glu Ser Ala Val Gly Val Ala Ala Leu Ala Lys Ala Gly Leu
62  290                295                300
63  Phe Tyr Thr Gly Ile Lys Asp Ile Val Gln Cys Phe Ser Cys Gly Gly
64  305                310                315                320
65  Cys Leu Glu Lys Trp Gln Glu Gly Asp Asp Pro Leu Asp Asp His Thr
66  325                330                335
67  Arg Cys Phe Pro Asn Cys Pro Phe Leu Gln Asn Met Lys Ser Ser Ala
68  340                345                350
69  Glu Val Thr Pro Asp Leu Gln Ser Arg Gly Glu Leu Cys Glu Leu Leu
70  355                360                365
71  Glu Thr Thr Ser Glu Ser Asn Leu Glu Asp Ser Ile Ala Val Gly Pro
72  370                375                380
73  Ile Val Pro Glu Met Ala Gln Gly Glu Ala Gln Trp Phe Gln Glu Ala
74  385                390                395                400
75  Lys Asn Leu Asn Glu Gln Leu Arg Ala Ala Tyr Thr Ser Ala Ser Phe
76  405                410                415
77  Arg His Met Ser Leu Leu Asp Ile Ser Ser Asp Leu Ala Thr Asp His
78  420                425                430
79  Leu Leu Gly Cys Asp Leu Ser Ile Ala Ser Lys His Ile Ser Lys Pro
80  435                440                445
81  Val Gln Glu Pro Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser
82  450                455                460
83  Val Met Cys Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu
84  465                470                475                480
85  Lys Lys Ile Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn
86  485                490                495
87  Arg Phe Gln Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp
88  500                505                510
89  Glu Gly Leu Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly
90  515                520                525
91  Ser Val Thr Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn
92  530                535                540
93  Gln Val Leu Phe Leu Leu Asp Asp Tyr Lys Glu Ile Cys Ser Ile Pro
94  545                550                555                560
95  Gln Val Ile Gly Lys Leu Ile Gln Lys Asn His Leu Ser Arg Thr Cys
96  565                570                575
97  Leu Leu Ile Ala Val Arg Thr Asn Arg Ala Arg Asp Ile Arg Arg Tyr
98  580                585                590
99  Leu Glu Thr Ile Leu Glu Ile Lys Ala Phe Pro Phe Tyr Asn Thr Val
100  595                600                605
101  Cys Ile Leu Arg Lys Leu Phe Ser His Asn Met Thr Arg Leu Arg Lys

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102	610	615	620
103	Phe Met Val Tyr Phe Gly Lys Asn Gln Ser Leu Gln Lys Ile Gln Lys		
104	625	630	635
105	Thr Pro Leu Phe Val Ala Ala Ile Cys Ala His Trp Phe Gln Tyr Pro		640
106		645	650
107	Phe Asp Pro Ser Phe Asp Asp Val Ala Val Phe Lys Ser Tyr Met Glu		655
108		660	665
109	Arg Leu Ser Leu Arg Asn Lys Ala Thr Ala Glu Ile Leu Lys Ala Thr		670
110		675	680
111	Val Ser Ser Cys Gly Glu Leu Ala Leu Lys Gly Phe Phe Ser Cys Cys		685
112	690	695	700
113	Phe Glu Phe Asn Asp Asp Asp Leu Ala Glu Ala Gly Val Asp Glu Asp		
114	705	710	715
115	Glu Asp Leu Thr Met Cys Leu Met Ser Lys Phe Thr Ala Gln Arg Leu		720
116		725	730
117	Arg Pro Phe Tyr Arg Phe Leu Ser Pro Ala Phe Gln Glu Phe Leu Ala		735
118		740	745
119	Gly Met Arg Leu Ile Glu Leu Leu Asp Ser Asp Arg Gln Glu His Gln		750
120		755	760
121	Asp Leu Gly Leu Tyr His Leu Lys Gln Ile Asn Ser Pro Met Met Thr		765
122	770	775	780
123	Val Ser Ala Tyr Asn Asn Phe Leu Asn Tyr Val Ser Ser Leu Pro Ser		
124	785	790	795
125	Thr Lys Ala Gly Pro Lys Ile Val Ser His Leu Leu His Leu Val Asp		800
126		805	810
127	Asn Lys Glu Ser Leu Glu Asn Ile Ser Glu Asn Asp Asp Tyr Leu Lys		815
128		820	825
129	His Gln Pro Glu Ile Ser Leu Gln Met Gln Leu Leu Arg Gly Leu Trp		830
130		835	840
131	Gln Ile Cys Pro Gln Ala Tyr Phe Ser Met Val Ser Glu His Leu Leu		845
132	850	855	860
133	Val Leu Ala Leu Lys Thr Ala Tyr Gln Ser Asn Thr Val Ala Ala Cys		
134	865	870	875
135	Ser Pro Phe Val Leu Gln Phe Leu Gln Gly Arg Thr Leu Thr Leu Gly		880
136		885	890
137	Ala Leu Asn Leu Gln Tyr Phe Phe Asp His Pro Glu Ser Leu Ser Leu		895
138		900	905
139	Leu Arg Ser Ile His Phe Pro Ile Arg Gly Asn Lys Thr Ser Pro Arg		910
140		915	920
141	Ala His Phe Ser Val Leu Glu Thr Cys Phe Asp Lys Ser Gln Val Pro		925
142	930	935	940
143	Thr Ile Asp Gln Asp Tyr Ala Ser Ala Phe Glu Pro Met Asn Glu Trp		
144	945	950	955
145	Glu Arg Asn Leu Ala Glu Lys Glu Asp Asn Val Lys Ser Tyr Met Asp		960
146		965	970
147	Met Gln Arg Arg Ala Ser Pro Asp Leu Ser Thr Gly Tyr Trp Lys Leu		975
148		980	985
149	Ser Pro Lys Gln Tyr Lys Ile Pro Cys Leu Glu Val Asp Val Asn Asp		990
150		995	1000
			1005

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151 Ile Asp Val Val Gly Gln Asp Met Leu Glu Ile Leu Met Thr Val Phe
152      1010      1015      1020
153 Ser Ala Ser Gln Arg Ile Glu Leu His Leu Asn His Ser Arg Gly Phe
154      1025      1030      1035      1040
155 Ile Glu Ser Ile Arg Pro Ala Leu Glu Leu Ser Lys Ala Ser Val Thr
156      1045      1050      1055
157 Lys Cys Ser Ile Ser Lys Leu Glu Leu Ser Ala Ala Glu Gln Glu Leu
158      1060      1065      1070
159 Leu Leu Thr Leu Pro Ser Leu Glu Ser Leu Glu Val Ser Gly Thr Ile
160      1075      1080      1085
161 Gln Ser Gln Asp Gln Ile Phe Pro Asn Leu Asp Lys Phe Leu Cys Leu
162      1090      1095      1100
163 Lys Glu Leu Ser Val Asp Leu Glu Gly Asn Ile Asn Val Phe Ser Val
164      1105      1110      1115      1120
165 Ile Pro Glu Glu Phe Pro Asn Phe His His Met Glu Lys Leu Leu Ile
166      1125      1130      1135
167 Gln Ile Ser Ala Glu Tyr Asp Pro Ser Lys Leu Val Lys Leu Ile Gln
168      1140      1145      1150
169 Asn Ser Pro Asn Leu His Val Phe His Leu Lys Cys Asn Phe Phe Ser
170      1155      1160      1165
171 Asp Phe Gly Ser Leu Met Thr Met Leu Val Ser Cys Lys Lys Leu Thr
172      1170      1175      1180
173 Glu Ile Lys Phe Ser Asp Ser Phe Phe Gln Ala Val Pro Phe Val Ala
174      1185      1190      1195      1200
175 Ser Leu Pro Asn Phe Ile Ser Leu Lys Ile Leu Asn Leu Glu Gly Gln
176      1205      1210      1215
177 Gln Phe Pro Asp Glu Glu Thr Ser Glu Lys Phe Ala Tyr Ile Leu Gly
178      1220      1225      1230
179 Ser Leu Ser Asn Leu Glu Glu Leu Ile Leu Pro Thr Gly Asp Gly Ile
180      1235      1240      1245
181 Tyr Arg Val Ala Lys Leu Ile Ile Gln Gln Cys Gln Gln Leu His Cys
182      1250      1255      1260
183 Leu Arg Val Leu Ser Phe Phe Lys Thr Leu Asn Asp Asp Ser Val Val
184      1265      1270      1275      1280
185 Glu Ile Ala Lys Val Ala Ile Ser Gly Gly Phe Gln Lys Leu Glu Asn
186      1285      1290      1295
187 Leu Lys Leu Ser Ile Asn His Lys Ile Thr Glu Glu Gly Tyr Arg Asn
188      1300      1305      1310
189 Phe Phe Gln Ala Leu Asp Asn Met Pro Asn Leu Gln Glu Leu Asp Ile
190      1315      1320      1325
191 Ser Arg His Phe Thr Glu Cys Ile Lys Ala Gln Ala Thr Thr Val Lys
192      1330      1335      1340
193 Ser Leu Ser Gln Cys Val Leu Arg Leu Pro Arg Leu Ile Arg Leu Asn
194      1345      1350      1355      1360
195 Met Leu Ser Trp Leu Leu Asp Ala Asp Asp Ile Ala Leu Leu Asn Val
196      1365      1370      1375
197 Met Lys Glu Arg His Pro Gln Ser Lys Tyr Leu Thr Ile Leu Gln Lys
198      1380      1385      1390
199 Trp Ile Leu Pro Phe Ser Pro Ile Ile Gln Lys

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200          1395          1400          1403
202 <210> SEQ ID NO: 2
203 <211> LENGTH: 5984
204 <212> TYPE: DNA
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
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209 <222> LOCATION: (292)..(4500)
211 <400> SEQUENCE: 2
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215 actgcttcct actaaaggac ggacagagca tttgttcttc agccacatac tttccttcca 240
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217 cagcagaaag cctctgacga gaggatctcc cagtttgatc acaatttgct gccagagctg 360
218 tctgctcttc tgggcctaga tgcagttcag ttggcaaagg aactagaaga agaggagcag 420
219 aaggagcgag caaaaatgca gaaaggctac aactctcaaa tgcgcagtga agcaaaaagg 480
220 ttaaagactt ttgtgactta tgagccgtac agctcatgga taccacagga gatggcggcc 540
221 gctgggtttt acttcaactgg ggtaaaatct gggattcagt gcttctgctg tagcctaate 600
222 ctctttgggtg ccggcctcac gagactcccc atagaagacc acaagagggtt tcatccagat 660
223 tgtgggttcc ttttgaacaa ggatgtttgt aacattgcca agtacgacat aaggggtgaag 720
224 aatctgaaga gcaggctgag aggaggtaaa atgaggtacc aagaagagga ggctagactt 780
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,338

DATE: 03/07/2002

TIME: 15:41:42

Input Set : A:\Ikeda Sequence Listing.txt

Output Set: N:\CRF3\03072002\I830338.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:212 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=2

FOR "0" SEQUENCE